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PAT 10-APR-2003
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Homo sapiens sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini; Hominidae, Homo.
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Best Local Similarity 100.0%; Pred. No. 5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 5.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 5.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels
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/organism='Unidentified'.
Location/Qualifiers
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AR267926.
AR267926.1 GI:29698051
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AX093873.1 GI:13510091
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Unclassified.
Unclassified.

1 (bases 1 to 28)
Cochran, M.D. and Junker, D.E.
Recombinant swinepox virus
Recombinant swinepox virus
AL Parent: US 649782-R 265 24 DEC
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PR 01-MAY-1999 US 09/071711
PR 01-MAY-1999 US 09/071711
PI BARBARA J WINSLOW, MARK D COCHRAN
PC C12AN5/09, A61X39/12, A61X39/125, A61X39/215, A61X39/215, PC A61X39/245,
PC A61X39/245,
PC A61X48/00, A61P43/00, C12N7/00//C07X14/705, C12N15/00 CC PIV
PPR downstream primer Location/Qualifiets
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Recombinant virus expressing foreign DNA encoding feline CD80,
Ealine DD86, feline CTLA-4 or feline interferon-gamma and uses
thereof.
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Sequence 84 from patent US 6221361.
AR147023.
AR147023.1 GI:1S110826
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BD273541.1 GI:33083309
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27 GGAAAGTAAAA 16
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:	March 25, 2004, 08:39:03 ; Search time 6718.14 Seconds (without alignments) 6361.316 Million cell updates/sec	
Title: Perfect score:	US-09-963-285-1_COPY_1250_2235	
Sequence: Scoring table:	i cigccartccaatccagogcgagocgtctcggaagca 985 IDENIIIY NUC Gapop 10 ⁷ 0 , Gapext 1.0	
Searched:	3470272 seqs, 21671516995 residues	
Total number of	Total number of hits satisfying chosen parameters: 6940544.	
Minimum DB seq] Maximum DB seq]	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	
Post-processing:	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database :	GenEmbl:* 1: gb_ba:* 2: qb_htq:*	

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BBBB P P C C C C C C C C C C C C C C C C

Miura N., lida, K., Kakinuma, H., Yang, X.L. and Sugiyama, T. **Existion of the mouse (MFH-1) and human (PKHL 14) mesenchyme fork head-1 genes reveals conservation of their gene and protein

REFERENCE AUTHORS TITLE

predicted by chance to have a

oca; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, ia; Eutheria; Primates; Catarrhini, Hominidae; Homo.

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ACOU9108 168656 bp DNA linear PRI 29-OCT-2002
Homo sapiens chromosome 16 clone RP11-46309, complete sequence.
ACO09108
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Dog Joint Genome Institute.

Direct Submission

Submitted (03-AUG-1999) Production Sequencing Facility, DOS Joint

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

Johases I to 16865)

DOE Joint Genome Institute, Stanford Human Genome Center and Los

Alamos National Laboratory.

Submitted (29-OCT-2002) DOE Joint Genome Institute, 2800 Mitchell
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bukaryota, Metazoa, Chordata, Cararhini, Hominidae, Homo.
1 (bases 1 to 16856)
DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
Direct Submission
CTCGGACCCCGGCGCGCTGACCTCGGGGCTGCCGATTCGCTGGGGGGCTTGGAGAGCCTC
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try, 1-1-1 Hondo, Akita 010, JAPAN
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Gene="Wiff-1"

foodon start=1

forduct="Mesenchyme Fork Head-1"

fprotein id="CAA69400.1"

fbrotein id="CAA69400.1"

fbrotein id="CAA: CAB9400.1"

fbrotein id="CAA: CAB958"

fbrotei="SAISS-PROT. CAB958"

franslation="MOARYSVSDPNALGVVPYLSEQNYYRAAGSYGGMASPMGVYSGH
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SPALPVITKVETLSPESALOGSPRSAASTPAGSPOGSLPEHHAAAPNGLPGFSVENIM
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AMSLYTGARPAHWCYPPALDBALSOPRSPSPYSPLSALNLAGGSGALAATGHHOCH
GHHBOAPPPPRAPOQPTPQPGAAAAAAASWYLNHSGDLNHLPGHTFRAQQOTPPNV
REMFINSHRLGIENSTLGESQVSGNASCQLPYRSTPPLYXHAAPYSYDCTKY"
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IDR F PFYRENKOGWONSIRHNLSLNBCFVKVPRDDKKPGKGSYWTLDPDSYNMFENGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              392 AATIGATITITITIAACAGAGAAAGIGGCIAICITITITITITITIGGGCAIGIGGGCCCAT 451
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100.0%; Score 986; DB 9; Length 3289;
Best Local Similarity 100.0%; Pred. No. 4.5e-169;
Matches 985; Conservative 0; Mismatches 0; Indels 0
                                                                                                        losses 1 to 3289)
Miura, N.
Direct Submission
Submitted (18-SEP-1996) N. Miura, Akita U
Medicine, Department of Biochemistry, 1-1
Location/Qualifiers
1, 3289
/ organism="Homo sapiens"
/ mol_type="genomic DNA"
/ db_tref="leaxon:9606"
| 1977. . 2702
         etructures
Genomice 41 (3), 489-492 (1997)
97312712
9169153
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                            JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
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REBULT 6
US-09-134-000C-1782/C
Squence 1782, Application US/09134000C
Squence 1782, Application US/09134000C
Squence 1782, Application US/09134000C
Target No. 6617156
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1998-08-15
PRIOR FILING DATE: 1997-08-15
SOFTWARE FRECHING DATE: 1997-08-15
SOFTWARE FRECHING VERSION 3.1
SEQ ID NO 1782
LENGTH: 381
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     Length 361;
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                                                0; Indels
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| Sequence 9538, Application US/09621976
| Sequence 9538, Application US/09621976
| Septent No. 6639063
| GENERAL INFORMATION:
| APPLICANT: Divert, S. APPLICANT: Glordano, J.Y. APPLICANT: Glordano, J.Y. APPLICANT: Glordano, J.Y. TITLE OF INVENTION: ESSE and Encoded Human Proteins. FILE REPRENCE: GENER. US/09/621, 976
| CURRENT PLINE DATE: 2000-07-21
| NUMBER OF SEO ID NOS: 19335
Query Match 100.0%; Score 12; DB 3; I Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 12; DB 4; Best Local Similarity 100.0%; Pred. No. 1.1e+03 Matches 12; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 12; DB 4; Best Local Similarity 100.0%; Pred. No. 1.1e+03 Matches 12; Conservative 0; Mismatches 0
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, Patent No. 6475739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            513 GGAAAGTAAAA 524
                                                                                                                                                  112 GGAAGTAAAA 101
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US-09-621-976-9538
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APPLICANT: Chumakov, Ilya
APPLICANT: Chan, Annick
IITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
FILE REPERENCE: 2000-05-27
CURRENT FILING DATE: 2000-05-27
PRIOR FILING DATE: 2000-03-23
PRIOR PLILING DATE: 2000-03-23
PRIOR PLILING DATE: 2000-03-24
PRIOR PLILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
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FILE REPERENCE: GTC39-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
SEQ ID NOS: 8252
SEQ ID NO 713
LENGTH: 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 12; DB 4; Length 602;
Best Local Similarity 100.0%; Pred. No. 1.14+03;
Matches 12; Conservative 0; Mismatches 0; Indels
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100.0%; Score 12; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 12; Conservative 0; Mismatches 0;
APPLICANT: Brunkow, Mary
APPLICANT: Proll, Sean
APPLICANT: Proll, Sean
APPLICANT: Paper, Bryan
APPLICANT: Stachling-Hampton, Karen
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: GROWIC DELETIONS
FILE REFERENCE: 240083.515
CURRENT APPLICATION NUMBER: US/09/918,686
CURRENT PILING DATE: 2011-07-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FRANCE OF Windows Version 4.0
LENGTH: 602
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Patent No. 6528260
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 713, Application US/09328352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ; ORGANISM: Acinetobacter baumannii US-09-328-352-713 **
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                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-686-7
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Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 9; Conservative 0; Mismatches 0; Indels
ZIP: 48641-1967

COMPUTER READABLE FORM:
MEDIUM TYPE: R.Dopy disk
COMPUTER: IBM PC compatible
SOFTWARE: PRICENTION DATA:
FILING DATE:
CLASSIFICATION NUMBER: US 08/040,687
FILING DATE:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: C-7,075C
REFERENCE/DOCKET NUMBER: C-7,075C
TELECOMMINION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 Dase Paris
                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-822-028-35
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                                                                                Sequence 19, Application 38/08512681
Fatern No. 5755976
GENERAL INFORMATION:
APPLICANT: Ocfiner, Perer J.
APPLICANT: Underhill, Perer A.
TITLE OF INVENTION: by Deneturing High Performance Liquid Chromatography and TITLE OF INVENTION: Methode for Comparative Sequencing NUMBERS OF SEQUENCES: 29 CORRESPONDENCE ADDRESS:
ADDRESSER: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: (MEZES PETER S
APPLICANT: CONTILE, BRIAN B
APPLICANT: RIXON WARK M
APPLICANT: ANDERSON, WH KERR
APPLICANT: KAPLAN, DONALD A
APPLICANT: SCHOLM, JEFFER APPLICANT: SCHOLM, JEFFER APPLICANT: SCHOLM, A NOVEL FAMILY OF RIGH APPINITY,
TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.04; Score 9; DB 1; Length 22;
Best Local Similarity 100.04; Pred. No. 2.8e+No. 3;
Matches 9; Conservative 0; Mismatches 0; Indels
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                         STATE: CA COUNTRY: USA ZIP: CA COUNTRY: USA ZIP: 94306
ZONFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM FC COMPATIBLE COMPUTER: IBM FC COMPATIBLE COMPUTER: PLOSS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE: WARRING MARER: US/06/512,681
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
COLECTUE TYPE: DNA
CORGUNAL SOURCE:
INDIVIDUAL ISOLATE: DY6234 REVERSE PRIMER
US-08-512-681-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INRORANTION:
NAME: Evans, Susan T.
REGISTRATION NUMBER: 36,443
REPERRICE/DOCKET NUMBER: 8600.
; INFORMATION FOR SEC ID NO: 5 SEQUENCE CHARACTERISTICS: 19: 5 SEQUENCE CHARACTERISTICS: 1 LENGTH: 22 base pairs
ITPE: nucleic acid
ITPE: nucleic acid
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STREET: P.O. BOX 1967
CITY: MICHIGAN
STATE: MICHIGAN
COUNTRY: USA
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                                                                       2-681-19/c
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Title: Perfect score:

Sequence:

OM nucleic

Scoring table:

Searched:

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Sequence 43641, A Sequence 256264, Sequence 256264, Sequence 24, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 2121, Appl Sequence 1366, Appl Sequence 1367, Appl Sequence 13677, Appl Sequen
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GERERAL IN PLANTERS.

TITLE OF INVENTION: POLYMOTPHISMS in the Human Genome
TITLE OF INVENTION: POLYMOTPHISMS in the Human Genome
TITLE OF INVENTION: POLYMOTPHISMS in the Human Genome
TITLE REFERENCE, 108 827.129
GURRENT APPLICATION NUMBER: US 60/218,006
FRIOR APPLICATION NUMBER: US 60/218,006
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR PLING DATE: 2000-04-120
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR PLING DATE: 2000-04-20
FRIOR APPLICATION NUMBER: US 60/195,188
FRIOR PLING DATE: 2000-04-20
FRIOR PLING DATE: 1099-11-23
FRIOR PLING DATE: 1099-11-23
FRIOR PLING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-8
FRIOR FRIOR FILING DATE: 1999-09-8
FRIOR FRIOR FRIOR PARIETER FRIOR FRI
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2. US-10-424-599-37752

10. US-10-424-599-43641

10. US-10-627-632-256263

10. US-10-027-632-256264

14. US-10-027-632-256264

15. US-10-087-080-24

15. US-10-087-080-24

15. US-10-274-177-12

16. US-10-274-177-12

17. US-10-274-177-12

18. US-10-082-186-13766

19. US-10-281-613-51

19. US-10-281-613-51

19. US-10-092-184-1369

19. US-10-093-184-1369

19. US-10-09
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Best Local Similarity 100.0
Matches 17; Conservative
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Sequence 17, Appl.
Sequence 10702, A
Sequence 10003, A
Sequence 977, App
Sequence 2718, Ap
Sequence 22032, A
Sequence 22032, A
Sequence 24033,
                                                                                                                                                                                                                                                                                                                                                                         March 25, 2004, 10:03:04; Search time 14.7262 Seconds (without alignments) 4297.861 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications NA: *

(cgn2 6/prodata/1/pubpna/USO7 pUBCOMB.seq: *

(cgn2 6/prodata/1/pubpna/DSO NEW PUB.seq: *

(cgn2 6/prodata/1/pubpna/USO6 NEW PUB.seq: *

(cgn2 6/prodata/1/pubpna/USO6 NEW PUB.seq: *

(cgn2 6/prodata/1/pubpna/USO7 NEW PUB.seq: *

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(cgn2 6/prodata/1/pubpna/USO8 NEW PUB.seq: *

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(cgn2 6/prodata/1/pubpna/USO8 PUBCOMB.seq: *

(cgn2 6/prodata/1/pubcomBuBCOMB.seq: *

(cgn2 6/prodata/1/pubcomBuBCOMB.seq: *

(cgn2 6/prodata/1/pubcomBuBCOMBuBCOMB.seq: *

(cgn2
                                                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-963-285-1

US-10-964-599-10702

2 US-10-424-599-10702

0 US-10-764-899-10003

4 US-10-205-428-918

5 US-10-424-599-64036

2 US-10-424-599-64036

2 US-10-424-599-22032

2 US-10-424-599-141232

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2458946 seqs, 1861504846 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-963-285-1_COPY_359_375
17
1 tgtggaaggaataaata 17
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Maximum Match 100*
Listing first 45 summaries
                                                                                                                                                                                                                                                                                     nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Query
Match Length DB
```

Score

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Sequence 8796, Application US/10424599
Sequence 8796, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21;53223) B
CURRENT APPLICANT: NUMBER: US/10/424,599
CURRENT FILING DATE: 2033-04-28
NUMBER OF SEQ ID NOS: 285684
ENGTH: 2521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10003, Application US/09764891
Sequence 10003, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acide, Proteins, and Antibodies;
TITLE OF INVENTION: Nucleic Acide, Proteins, and Antibodies;
TITLE PERFERENCE: PCO06
CURRENT APPLICATION WINGER: US/09/764,891
PRIOR APPLICATION UNGER: US/09/764,891
PRIOR APPLICATION UNGER: US/09/764,891
SEQ ID NO: 10.001
SEQ ID NO: 10.003
LENGTH: 21619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

94.1%; Score 16; DB 12; Length 25

Best Local Similarity 100.0%; Pred. No. 5.2e+02;

Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
CTHER INFORMATION: Clone ID: PAT_MRT3847_45782C.1
US-10-424-599-82796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          602 drácaácsártaatá 617
                                                                         233 GTGGAAGGAATAATA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GTGGAAGGAATAATA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Glycine max
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100.0%; Score 17; DB 9; Length 6458;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels (
                                                                                                                                       US-US-Y85-285-1
Sequence 1, Application US/05963285
FRACENT NO. US2002009707A1
GENERAL INFORMATION:
APPLICANT: Encick, Sven
APPLICANT: Excok, Katarina
APPLICANT: ROOK, Katarina
APPLICANT: ROOK, Katarina
APPLICANT: RODGHI, Lene
TILLE OF INVENTION: PROMOTER EQUENCES
FILE REPERENCE: 13425-042001
CURRENT APPLICATION NUMBER: US/09/963,285
FRIOR APPLICATION NUMBER: SE 0004102-0
FRIOR APPLICATION NUMBER: US 60/238,897
FRIOR APPLICATION NUMBER: US 60/238,897
FRIOR APPLICATION NUMBER: US 60/238,897
FRIOR FILING DATE: 2000-10-10
FRIOR FILING DATE: 2000-10-10
FRIOR FILING DATE: 2000-09-26
NUMBER OF FRIOR DATE: 2000-09-26
NUMBER: FRIESEQ for Windows Version 4.0
SEQ ID NO 1
ENGINE 648
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 TGTGGAAGGAATAAATA 375
127 TGTGGAAGGAATAATA 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TGTGGAAGGAATAAATA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:

NAME/KEY: CDS

LOCATION: (2235)...(3737)

US-09-963-285-1
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Query Match 94.1%; Score 16; DB 10; Length 21 Best Local Similarity 100.0%; Pred. No. 6.5e+02; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                1 TGTGGAAGGAATAAT 16
TYPE: DNA
ORGANISM: Homo sapiens
                                                         US-09-764-891-10003
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US-10424-599-107702

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US-10-205-428-977/c

Sequence 977, Application US/10205428

Sequence 977, Coronal Coro
SELO TGTGGAAGGAATAAAT 5295
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Query Match

94.1%; Score 16; DB 12; Length 493;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;

Matches 16; Conservative 0; Mismatches 0; Indels

ö

FEATURE:
NAMB/KES;
NAMB/KES;
LOCATION: (1)..(493)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_68271C.1
US-10-424-599.107702

TYPE: DNA ORGANISM: Glycine max